

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 10/6/7, 835  
Source: 1FW0  
Date Processed by STIC: 2/17/05

# ***ENTERED***

## CRF Errors Edited by the STIC Systems Branch

Serial Number: 10/6/7,835

CRF Edit Date: 2/17/05  
Edited by: AR

\_\_\_ Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line

\_\_\_ Corrected the SEQ ID NO. Sequence numbers edited were:

\_\_\_\_\_

\_\_\_ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

\_\_\_\_\_

\_\_\_ Deleted: \_\_\_ invalid beginning/end-of-file text ; \_\_\_ page numbers

\_\_\_ Inserted mandatory headings/numeric identifiers, specifically:

\_\_\_\_\_

\_\_\_ Moved responses to same line as heading/numeric identifier, specifically:

\_\_\_\_\_

Other: Sequence 2 - Deleted <2117 - <2137 lines and  
"this sequence is intentionally skipped" line



IFWO

## RAW SEQUENCE LISTING

DATE: 02/17/2005

PATENT APPLICATION: US/10/617,835

TIME: 12:24:18

Input Set : N:\Crif3\RULE60\10617835.raw

Output Set: N:\CRF4\02172005\J617835.raw

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1 <110> APPLICANT: MEYER, Thomas F.
2     RUDEL, Thomas
3     SCHEUERPFUG, Ina
4     MAIER, Jorgen
5     EICKERNJAGER, Sandra
6     SCHWAN, Thomas
7 <120> TITLE OF INVENTION: Nucleic Acid Molecules Encoding Proteins Which Impart
8     the Adhesion of Neisseria Cells to Human Cells
9 <130> FILE REFERENCE: 0147-172P
10 <140> CURRENT APPLICATION NUMBER: US/10/617,835
11 <141> CURRENT FILING DATE: 2003-07-14
12 <150> PRIOR APPLICATION NUMBER: US/09/043,302
13 <151> PRIOR FILING DATE: 1998-06-08
14 <150> PRIOR APPLICATION NUMBER: PCT/EP96/04092
15 <151> PRIOR FILING DATE: 1995-09-18
16 <160> NUMBER OF SEQ ID NOS: 11
17 <170> SOFTWARE: PatentIn Ver. 2.0
19 <210> SEQ ID NO: 1
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21 <212> TYPE: DNA
22 <213> ORGANISM: Neisseria gonorrhoeae
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25 <222> LOCATION: (136)..(447)
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27 <221> NAME/KEY: CDS
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34     cttcagacgg catttttata ataaggcgct gtcctagata actagggaaa ttcaaattaa 120
35     gttagaatta tccct atg aga aaa agc cgt cta agc cgg tat aaa caa aat 171
36             Met Arg Lys Ser Arg Leu Ser Arg Tyr Lys Gln Asn
37             1             5             10
38     aaa ctc att gaa ctg ttt gtc gca ggc gta act gca aga aca gca gca 219
39     Lys Leu Ile Glu Leu Phe Val Ala Gly Val Thr Ala Arg Thr Ala Ala
40             15             20             25
41     gag cct gac agc att gtt tat acg gat tgt tat cgt cgc tat gat gta 267
42     Glu Pro Asp Ser Ile Val Tyr Thr Asp Cys Tyr Arg Arg Tyr Asp Val
43             30             35             40
44     ttg gat gcg ggc gaa ttt agc cat ttc cgt atc aat cac agc aca cat 315

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Input Set : N:\Crif3\RULE60\10617835.raw

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45   Leu Asp Ala Gly Glu Phe Ser His Phe Arg Ile Asn His Ser Thr His
46       45                50                55                60
47   ttt gcc gaa cga caa aac cat att aat gga att ggg aac ttt tgg aac   363
48   Phe Ala Glu Arg Gln Asn His Ile Asn Gly Ile Gly Asn Phe Trp Asn
49               65                70                75
50   cgg gca aaa cgt cat tta cgc aag ttt gac ggc att ccc aaa gag cat   411
51   Arg Ala Lys Arg His Leu Arg Lys Phe Asp Gly Ile Pro Lys Glu His
52               80                85                90
53   ttt gag ccg tat tta aag gag tgc gaa cgg cgt ttt taacaacagt   457
54   Phe Glu Pro Tyr Leu Lys Glu Cys Glu Arg Arg Phe
55       95                100
56   gagataaaag ttcttgttcc attttaaaac aattagtaaa atcgagttaa tcctagtgt   517
57   ccaggacggc ccctaattta tttaacaattt tgatacaatt tgtttttcat caaaggagaa   577
58   aatct atg cgg gca cgg ctg ctg ata cct att ctt ttt tcg gtt ttt att   627
59       Met Arg Ala Arg Leu Leu Ile Pro Ile Leu Phe Ser Val Phe Ile
60       105                110                115
61   tta tcc gcc tgc ggg aca ctg aca ggt att cca tcg cat ggc gga ggc   675
62   Leu Ser Ala Cys Gly Thr Leu Thr Gly Ile Pro Ser His Gly Gly Gly
63       120                125                130                135
64   aaa cgc ttc gcg gtc gaa caa gaa ctt gtg gcc gct tct gcc aga gct   723
65   Lys Arg Phe Ala Val Glu Gln Glu Leu Val Ala Ala Ser Ala Arg Ala
66               140                145                150
67   gcc gtt aaa gac atg gat tta cag gca tta cac gga cga aaa gtt gca   771
68   Ala Val Lys Asp Met Asp Leu Gln Ala Leu His Gly Arg Lys Val Ala
69               155                160                165
70   ttg tac att gca act atg ggc gac caa ggt tca ggc agt ttg aca ggg   819
71   Leu Tyr Ile Ala Thr Met Gly Asp Gln Gly Ser Gly Ser Leu Thr Gly
72               170                175                180
73   ggt cgc tac tcc att gat gca ctg att cgc ggc gaa tac ata aac agc   867
74   Gly Arg Tyr Ser Ile Asp Ala Leu Ile Arg Gly Glu Tyr Ile Asn Ser
75               185                190                195
76   cct gcc gtc cgc acc gat tac acc tat ccg cgt tac gaa acc acc gct   915
77   Pro Ala Val Arg Thr Asp Tyr Thr Tyr Pro Arg Tyr Glu Thr Thr Ala
78       200                205                210                215
79   gaa aca aca tca ggc ggt ttg acg ggt tta acc act tct tta tct aca   963
80   Glu Thr Thr Ser Gly Gly Leu Thr Gly Leu Thr Thr Ser Leu Ser Thr
81               220                225                230
82   ctt aat gcc cct gca ctc tcg cgc acc caa tca gac ggt agc gga agt   1011
83   Leu Asn Ala Pro Ala Leu Ser Arg Thr Gln Ser Asp Gly Ser Gly Ser
84               235                240                245
85   agg agc agt ctg ggc tta aat att ggc ggg atg ggg gat tat cga aat   1059
86   Arg Ser Ser Leu Gly Leu Asn Ile Gly Gly Met Gly Asp Tyr Arg Asn
87               250                255                260
88   gaa acc ttg acg acc aac ccg cgc gac act gcc ttt ctt tcc cac ttg   1107
89   Glu Thr Leu Thr Thr Asn Pro Arg Asp Thr Ala Phe Leu Ser His Leu
90       265                270                275
91   gta cag acc gta ttt ttc ctg cgc ggc ata gac gtt gtt tct cct gcc   1155
92   Val Gln Thr Val Phe Phe Leu Arg Gly Ile Asp Val Val Ser Pro Ala
93       280                285                290                295

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Input Set : N:\Crif3\RULE60\10617835.raw

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94  aat gcc gat aca gat gtg ttt att aac atc gac gta ttc gga acg ata 1203
95  Asn Ala Asp Thr Asp Val Phe Ile Asn Ile Asp Val Phe Gly Thr Ile
96          300          305          310
97  cgc aac aga acc gaa atg cac cta tac aat gcc gaa aca ctg aaa gcc 1251
98  Arg Asn Arg Thr Glu Met His Leu Tyr Asn Ala Glu Thr Leu Lys Ala
99          315          320          325
100  caa aca aaa ctg gaa tat ttc gca gta gac aga acc aat aaa aaa ttg 1299
101  Gln Thr Lys Leu Glu Tyr Phe Ala Val Asp Arg Thr Asn Lys Lys Leu
102          330          335          340
103  ctc atc aaa ccc aaa acc aat gcg ttt gaa gct gcc tat aaa gaa aat 1347
104  Leu Ile Lys Pro Lys Thr Asn Ala Phe Glu Ala Ala Tyr Lys Glu Asn
105          345          350          355
106  tac gca ttg tgg atg ggg ccg tat aaa gta agc aaa gga atc aaa ccg 1395
107  Tyr Ala Leu Trp Met Gly Pro Tyr Lys Val Ser Lys Gly Ile Lys Pro
108          360          365          370          375
109  acg gaa gga tta atg gtc gat ttc tcc gat atc cgg cca tac ggc aat 1443
110  Thr Glu Gly Leu Met Val Asp Phe Ser Asp Ile Arg Pro Tyr Gly Asn
111          380          385          390
112  cat acg ggt aac tcc gcc cca tcc gta gag gct gat aac agt cat gag 1491
113  His Thr Gly Asn Ser Ala Pro Ser Val Glu Ala Asp Asn Ser His Glu
114          395          400          405
115  ggg tat gga tac agc gat gaa gca gtg cga caa cat aga caa ggg caa 1539
116  Gly Tyr Gly Tyr Ser Asp Glu Ala Val Arg Gln His Arg Gln Gly Gln
117          410          415          420
118  cct tgattcacac tgccataacc gcttgctgcc aaggaaaaca aa atg aat ttg 1593
119  Pro          Met Asn Leu
120          425
121  cct att caa aaa ttc atg atg ctg ttt gca gcg gca ata tcg ttg ctg 1641
122  Pro Ile Gln Lys Phe Met Met Leu Phe Ala Ala Ala Ile Ser Leu Leu
123          430          435          440
124  caa atc ccc att agt cat gcg aac ggt ttg gat gcc cgt ttg cgc gat 1689
125  Gln Ile Pro Ile Ser His Ala Asn Gly Leu Asp Ala Arg Leu Arg Asp
126          445          450          455
127  gat atg cag gca aaa cac tac gaa ccg ggt ggc aaa tac cat ctg ttc 1737
128  Asp Met Gln Ala Lys His Tyr Glu Pro Gly Gly Lys Tyr His Leu Phe
129          460          465          470          475
130  ggt aat gct cgc ggc agt gtt aaa aat cgg gtt tgc gcc gtc caa aca 1785
131  Gly Asn Ala Arg Gly Ser Val Lys Asn Arg Val Cys Ala Val Gln Thr
132          480          485          490
133  ttt gat gca act gcg gtc ggc ccc ata ctg cct att aca cac gaa cgg 1833
134  Phe Asp Ala Thr Ala Val Gly Pro Ile Leu Pro Ile Thr His Glu Arg
135          495          500          505
136  aca ggg ttt gaa ggc att atc ggt tat gaa acc cat ttt tca gga cac 1881
137  Thr Gly Phe Glu Gly Ile Ile Gly Tyr Glu Thr His Phe Ser Gly His
138          510          515          520
139  gga cac gaa gta cac agt ccg ttc gat aat cat gat tca aaa agc act 1929
140  Gly His Glu Val His Ser Pro Phe Asp Asn His Asp Ser Lys Ser Thr
141          525          530          535
142  tct gat ttc agc ggc ggc gta gac ggc ggt ttt acc gtt tac caa ctt 1977

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Input Set : N:\Crif3\RULE60\10617835.raw

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143	Ser	Asp	Phe	Ser	Gly	Gly	Val	Asp	Gly	Gly	Phe	Thr	Val	Tyr	Gln	Leu	
144	540					545					550					555	
145	cat	cgg	aca	ggg	tcg	gaa	ata	cat	ccc	gca	gac	gga	tat	gac	ggg	cct	2025
146	His	Arg	Thr	Gly	Ser	Glu	Ile	His	Pro	Ala	Asp	Gly	Tyr	Asp	Gly	Pro	
147				560						565					570		
148	caa	ggc	ggc	ggg	tat	ccg	gaa	cca	caa	ggg	gca	agg	gat	ata	tac	agc	2073
149	Gln	Gly	Gly	Gly	Tyr	Pro	Glu	Pro	Gln	Gly	Ala	Arg	Asp	Ile	Tyr	Ser	
150				575						580					585		
151	tac	cat	atc	aaa	gga	act	tca	acc	aaa	aca	aag	ata	aac	act	gtt	ccg	2121
152	Tyr	His	Ile	Lys	Gly	Thr	Ser	Thr	Lys	Thr	Lys	Ile	Asn	Thr	Val	Pro	
153				590					595					600			
154	caa	gcc	cct	ttt	tca	gac	cgc	tgg	cta	aaa	gaa	aat	gcc	ggg	gcc	gct	2169
155	Gln	Ala	Pro	Phe	Ser	Asp	Arg	Trp	Leu	Lys	Glu	Asn	Ala	Gly	Ala	Ala	
156				605					610					615			
157	tcc	ggg	ttt	ctc	agc	cgt	gcg	gat	gaa	gca	gga	aaa	ctg	ata	tgg	gaa	2217
158	Ser	Gly	Phe	Leu	Ser	Arg	Ala	Asp	Glu	Ala	Gly	Lys	Leu	Ile	Trp	Glu	
159						625					630					635	
160	aac	gac	ccc	gat	aaa	aat	tgg	cgg	gct	aac	cgt	atg	gat	gat	att	cgc	2265
161	Asn	Asp	Pro	Asp	Lys	Asn	Trp	Arg	Ala	Asn	Arg	Met	Asp	Asp	Ile	Arg	
162					640						645					650	
163	ggc	atc	gtc	caa	ggg	gcg	ggt	aat	cct	ttt	tta	acg	ggg	ttt	cag	gga	2313
164	Gly	Ile	Val	Gln	Gly	Ala	Val	Asn	Pro	Phe	Leu	Thr	Gly	Phe	Gln	Gly	
165				655						660						665	
166	ttg	gga	ggt	ggg	gca	att	aca	gac	agt	gcg	gta	agc	ccg	gta	acc	tat	2361
167	Leu	Gly	Val	Gly	Ala	Ile	Thr	Asp	Ser	Ala	Val	Ser	Pro	Val	Thr	Tyr	
168				670						675					680		
169	gcg	gca	gca	cgg	aaa	act	tta	cag	ggg	att	cac	aat	tta	gga	aat	tta	2409
170	Ala	Ala	Ala	Arg	Lys	Thr	Leu	Gln	Gly	Ile	His	Asn	Leu	Gly	Asn	Leu	
171				685										695			
172	agt	ccg	gaa	gca	caa	ctt	gcc	gcc	gcg	agc	cta	tta	cag	gac	agt	gcc	2457
173	Ser	Pro	Glu	Ala	Gln	Leu	Ala	Ala	Ala	Ser	Leu	Leu	Gln	Asp	Ser	Ala	
174						705								710		715	
175	ttt	gcg	gta	aaa	gac	ggc	atc	aat	tcc	gcc	aga	caa	tgg	gct	gat	gcc	2505
176	Phe	Ala	Val	Lys	Asp	Gly	Ile	Asn	Ser	Ala	Arg	Gln	Trp	Ala	Asp	Ala	
177					720						725					730	
178	cat	ccg	aat	ata	aca	gca	aca	gcc	caa	act	gcc	ctt	gcc	gta	gca	gag	2553
179	His	Pro	Asn	Ile	Thr	Ala	Thr	Ala	Gln	Thr	Ala	Leu	Ala	Val	Ala	Glu	
180				735							740					745	
181	gct	gca	ggg	acg	ggt	tgg	gga	ggg	aaa	aaa	gta	gaa	ctt	aac	ccg	acc	2601
182	Ala	Ala	Gly	Thr	Val	Trp	Gly	Gly	Lys	Lys	Val	Glu	Leu	Asn	Pro	Thr	
183				750							755					760	
184	aaa	tgg	gat	tgg	ggt	aaa	aat	acc	ggc	tat	gaa	aaa	cct	gct	gcc	cga	2649
185	Lys	Trp	Asp	Trp	Val	Lys	Asn	Thr	Gly	Tyr	Glu	Lys	Pro	Ala	Ala	Arg	
186				765										775			
187	cct	atg	cag	act	gta	gac	ggg	gaa	atg	gcc	ggg	aaa	aat	aag	cca	ccg	2697
188	Pro	Met	Gln	Thr	Val	Asp	Gly	Glu	Met	Ala	Gly	Lys	Asn	Lys	Pro	Pro	
189						785								790		795	
190	aaa	cca	agt	acg	cag	caa	cac	tct	aca	cac	tct	gat	aac	aat	atc	ggc	2745
191	Lys	Pro	Ser	Thr	Gln	Gln	His	Ser	Thr	His	Ser	Asp	Asn	Asn	Ile	Gly	

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Input Set : N:\Crif3\RULE60\10617835.raw

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193      tta cct gcc cca tat gtt aaa cct gat aca tct att tct ccg aca gga 2793
194      Leu Pro Ala Pro Tyr Val Lys Pro Asp Thr Ser Ile Ser Pro Thr Gly
195          815          820          825
196      aca att caa gac cgc atc aga tgg aca aaa tcc aag ttt cct act gag 2841
197      Thr Ile Gln Asp Arg Ile Arg Trp Thr Lys Ser Lys Phe Pro Thr Glu
198          830          835          840
199      aaa tct tta aat gga cat ttc aaa gct cat gga aaa gaa ttt ggc gat 2889
200      Lys Ser Leu Asn Gly His Phe Lys Ala His Gly Lys Glu Phe Gly Asp
201          845          850          855
202      ata acc att gaa gac tac caa aaa atg gcg tct gat ttg tta tca aaa 2937
203      Ile Thr Ile Glu Asp Tyr Gln Lys Met Ala Ser Asp Leu Leu Ser Lys
204      860          865          870          875
205      cag aca tcg gac aag ata tta ggt tat cag acg gaa cat aga cga gtg 2985
206      Gln Thr Ser Asp Lys Ile Leu Gly Tyr Gln Thr Glu His Arg Arg Val
207          880          885          890
208      cgc tat gat atc aat aac aat atc tat gtt ttg gcc aat cca aaa aca 3033
209      Arg Tyr Asp Ile Asn Asn Asn Ile Tyr Val Leu Ala Asn Pro Lys Thr
210          895          900          905
211      ttc aaa atc aaa aca atg ttt aaa cca aac tta gga aag gag tat tat 3081
212      Phe Lys Ile Lys Thr Met Phe Lys Pro Asn Leu Gly Lys Glu Tyr Tyr
213          910          915          920
214      gat gga gaa ttc aaa aaa gac atg gga aat tgacggagaa atatggctac 3131
215      Asp Gly Glu Phe Lys Lys Asp Met Gly Asn
216          925          930
217      attgtcctgt ttgcggaact gaagttatgg actatgatat ctgtgacgtt tgtcagtggc 3191
218      aaaatacagg agaaactaat atagatggtg gtctaatga aatgacactt gcggaggcga 3251
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222 <400> SEQUENCE: 2
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226 <211> LENGTH: 104
227 <212> TYPE: PRT
228 <213> ORGANISM: Neisseria gonorrhoeae
229 <400> SEQUENCE: 3
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233          20          25          30
234      Ile Val Tyr Thr Asp Cys Tyr Arg Arg Tyr Asp Val Leu Asp Ala Gly
235          35          40          45
236      Glu Phe Ser His Phe Arg Ile Asn His Ser Thr His Phe Ala Glu Arg
237          50          55          60
238      Gln Asn His Ile Asn Gly Ile Gly Asn Phe Trp Asn Arg Ala Lys Arg
239          65          70          75          80
240      His Leu Arg Lys Phe Asp Gly Ile Pro Lys Glu His Phe Glu Pro Tyr
241          85          90          95
242      Leu Lys Glu Cys Glu Arg Arg Phe

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**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/617,835

DATE: 02/17/2005

TIME: 12:24:19

Input Set : N:\Cr3\RULE60\10617835.raw

Output Set: N:\CRF4\02172005\J617835.raw

L:223 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (2) SEQUENCE:





IFWO

**RAW SEQUENCE LISTING**

DATE: 02/17/2005

PATENT APPLICATION: US/10/617,835

TIME: 12:16:55

Input Set : N:\Crf3\RULE60\10617835.raw.txt

Output Set: N:\CRF4\02172005\J617835.raw

1 <110> APPLICANT: MEYER, Thomas F.  
 2 RUDEL, Thomas  
 3 SCHEUERPFUG, Ina  
 4 MAIER, Jorgen  
 5 EICKERNJAGER, Sandra  
 6 SCHWAN, Thomas  
 7 <120> TITLE OF INVENTION: Nucleic Acid Molecules Encoding Proteins Which Impart  
 8 the Adhesion of Neisseria Cells to Human Cells  
 9 <130> FILE REFERENCE: 0147-172P  
 10 <140> CURRENT APPLICATION NUMBER: US/10/617,835  
 11 <141> CURRENT FILING DATE: 2003-07-14  
 12 <150> PRIOR APPLICATION NUMBER: US/09/043,302  
 13 <151> PRIOR FILING DATE: 1998-06-08  
 14 <150> PRIOR APPLICATION NUMBER: PCT/EP96/04092  
 15 <151> PRIOR FILING DATE: 1995-09-18  
 16 <160> NUMBER OF SEQ ID NOS: 11  
 17 <170> SOFTWARE: PatentIn Ver. 2.0

**Does Not Comply  
Corrected Diskette Needed**

**ERRORED SEQUENCES**

221 <210> SEQ ID NO: 2  
 222 <211> LENGTH: *delete*  
 223 <212> TYPE:  
 224 <213> ORGANISM:  
 E--> 225 <400> SEQUENCE: 2  
 226 ~~This Sequence is intentionally skipped~~ *delete*

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/617,835

DATE: 02/17/2005

TIME: 12:16:56

Input Set : N:\Crf3\RULE60\10617835.raw.txt

Output Set: N:\CRF4\02172005\J617835.raw

L:225 M:210 E: (40) Invalid Number of Sequences, LENGTH:

L:225 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:

L:225 M:201 W: Mandatory field data missing, <213> ORGANISM